

RAW SEQUENCE LISTING

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Application Serial Number: 10/809,953A
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/809,953A

DATE: 08/01/2006

TIME: 09:46:26

Input Set : A:\1021565-000155.ST25.txt

Output Set: N:\CRF4\08012006\J809953A.raw

3 <110> APPLICANT: Van Mellaert, Herman
 4 Botterman, Johan
 5 Van Rie, Jeroen
 6 Joos, Henk
 8 <120> TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY
 BINDING Bt
 9 INSECTICIDAL CRYSTAL PROTEINS
 11 <130> FILE REFERENCE: 1021565-000155
 13 <140> CURRENT APPLICATION NUMBER: 10/809,953A
 14 <141> CURRENT FILING DATE: 2004-03-26
 16 <150> PRIOR APPLICATION NUMBER: 09/661,061
 17 <151> PRIOR FILING DATE: 2000-09-13
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP/00905
 20 <151> PRIOR FILING DATE: 1990-05-30
 22 <150> PRIOR APPLICATION NUMBER: GB 89401499.2
 23 <151> PRIOR FILING DATE: 1989-05-31
 25 <160> NUMBER OF SEQ ID NOS: 10
 27 <170> SOFTWARE: PatentIn version 3.3
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 12
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Bacillus thuringiensis
 34 <400> SEQUENCE: 1
 35 tggccagcgc ca 12
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 15
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Bacillus thuringiensis
 43 <400> SEQUENCE: 2 15
 44 tgccagcgcc accat
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 28
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Bacillus thuringiensis
 52 <400> SEQUENCE: 3
 53 cggaggtatt ccatgggaga aaataatc 28
 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 34
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Bacillus thuringiensis
 61 <400> SEQUENCE: 4
 62 cctatttgaa gccatggtaa ctcctccttt tatg 34
 65 <210> SEQ ID NO: 5
 66 <211> LENGTH: 3903

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67 <212> TYPE: DNA
 68 <213> ORGANISM: *Bacillus thuringiensis*
 71 <220> FEATURE:
 72 <221> NAME/KEY: CDS
 73 <222> LOCATION: (264) .. (3761)
 75 <400> SEQUENCE: 5

76 ggatctgttt taatataagg gatttgtgcc cttctcgta tattcttta tttagccccaa	60
78 aaactagtgc aactaaatat tttataatt acactgatta aatactttat ttttggaggt	120
80 aagatttatg ctgaaatgta ataaaattcg ttccattttc tgtatTTCT cataaaatgt	180
82 ttcatatgct ttaaattgta gtaaagaaaa acagtacaaa cttaaaagga cttagtaat	240
84 ttaataaaaa aaggggatag ttt atg gaa ata aat aat caa aac caa tgt gtg	293
85 Met Glu Ile Asn Asn Gln Asn Gln Cys Val	
86 1 5 10	
88 cct tac aat tgt tta agt aat cct aag gag ata ata tta ggc gag gaa	341
89 Pro Tyr Asn Cys Leu Ser Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu	
90 15 20 25	
92 agg cta gaa aca ggg aat act gta gca gac att tca tta ggg ctt att	389
93 Arg Leu Glu Thr Gly Asn Thr Val Ala Asp Ile Ser Leu Gly Leu Ile	
94 30 35 40	
96 aat ttt cta tat tct aat ttt gta cca gga gga gga ttt ata gta ggt	437
97 Asn Phe Leu Tyr Ser Asn Phe Val Pro Gly Gly Phe Ile Val Gly	
98 45 50 55	
100 tta cta gaa tta ata tgg gga ttt ata ggg cct tcg caa tgg gat att	485
101 Leu Leu Glu Leu Ile Trp Gly Phe Ile Gly Pro Ser Gln Trp Asp Ile	
102 60 65 70	
104 ttt tta gctcaa att gag caa ttg att agt caa aga ata gaa gaa ttt	533
105 Phe Leu Ala Gln Ile Glu Gln Leu Ile Ser Gln Arg Ile Glu Glu Phe	
106 75 80 85 90	
108 gct agg aat caq gca att tca aga ttg qag ggg cta agc aat ctt tat	581
109 Ala Arg Asn Gln Ala Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr	
110 95 100 105	
112 aag gtc tat gtt aga gcg ttt agc gac tgg gag aaa gat cct act aat	629
113 Lys Val Tyr Val Arg Ala Phe Ser Asp Trp Glu Lys Asp Pro Thr Asn	
114 110 115 120	
116 cct gct tta agg gaa atg cgt ata caa ttt aat gac atg aat agt	677
117 Pro Ala Leu Arg Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser	
118 125 130 135	
120 gct ctc ata acg gct att cca ctt ttt aga gtt caa aat tat gaa gtt	725
121 Ala Leu Ile Thr Ala Ile Pro Leu Phe Arg Val Gln Asn Tyr Glu Val	
122 140 145 150	
124 gct ctt tta tct gta tat gtt caa gcc gca aac tta cat tta tct att	773
125 Ala Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu Ser Ile	
126 155 160 165 170	
128 tta agg gat gtt tca gtt ttc qga gaa aga tgg gga tat gat aca gcg	821
129 Leu Arg Asp Val Ser Val Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala	
130 175 180 185	
132 act atc aat aat cgc tat agt gat ctg act agc ctt att cat gtt tat	869
133 Thr Ile Asn Asn Arg Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr	
134 190 195 200	

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136	act aac cat tgt gtg gat acg tat aat cag gga tta agg cgt ttg gaa	917
137	Thr Asn His Cys Val Asp Thr Tyr Asn Gln Gly Leu Arg Arg Leu Glu	
138	205 210 215	
140	ggt cgt ttt ctt agc gat tgg att gta tat aat cgt ttc cgg aga caa	965
141	Gly Arg Phe Leu Ser Asp Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln	
142	220 225 230	
144	ttg aca att tca gta tta gat att gtt gcg ttt ttt cca aat tat gat	1013
145	Leu Thr Ile Ser Val Leu Asp Ile Val Ala Phe Phe Pro Asn Tyr Asp	
146	235 240 245 250	
148	att aga aca tat cca att caa aca gct act cag cta acg agg gaa gtc	1061
149	Ile Arg Thr Tyr Pro Ile Gln Thr Ala Thr Gln Leu Thr Arg Glu Val	
150	255 260 265	
152	tat ctg gat tta cct ttt att aat caa aat ctt tct cct gca gca agc	1109
153	Tyr Leu Asp Leu Pro Phe Ile Asn Gln Asn Leu Ser Pro Ala Ala Ser	
154	270 275 280	
156	tat cca acc ttt tca gct gct gaa agt gct ata att aga agt cct cat	1157
157	Tyr Pro Thr Phe Ser Ala Ala Glu Ser Ala Ile Ile Arg Ser Pro His	
158	285 290 295	
160	tta gta gac ttt tta aat agc ttt acc att tat aca gat agt ctg gca	1205
161	Leu Val Asp Phe Leu Asn Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala	
162	300 305 310	
164	cgt tat gca tat tgg gga ggg cac ttg gta aat tct ttc cgc aca gga	1253
165	Arg Tyr Ala Tyr Trp Gly Gly His Leu Val Asn Ser Phe Arg Thr Gly	
166	315 320 325 330	
168	acc act act aat ttg ata aga tcc cct tta tat gga agg gaa gga aat	1301
169	Thr Thr Thr Asn Leu Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn	
170	335 340 345	
172	aca gag cgc ccc gta act att acc gca tca cct agc gta cca ata ttt	1349
173	Thr Glu Arg Pro Val Thr Ile Thr Ala Ser Pro Ser Val Pro Ile Phe	
174	350 355 360	
176	aga aca ctt tca tat att aca ggc ctt gac aat tca aat cct gta gct	1397
177	Arg Thr Leu Ser Tyr Ile Thr Gly Leu Asp Asn Ser Asn Pro Val Ala	
178	365 370 375	
180	gga atc gag gga gtg gaa ttc caa aat act ata agt aga agt atc tat	1445
181	Gly Ile Glu Gly Val Glu Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr	
182	380 385 390	
184	cgt aaa agc ggt cca ata gat tct ttt agt gaa tta cca cct caa gat	1493
185	Arg Lys Ser Gly Pro Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp	
186	395 400 405 410	
188	gcc agc gta tct cct gca att ggg tat agt cac cgt tta tgc cat gca	1541
189	Ala Ser Val Ser Pro Ala Ile Gly Tyr Ser His Arg Leu Cys His Ala	
190	415 420 425	
192	aca ttt tta gaa cgg att agt gga cca aga ata gca ggc acc gta ttt	1589
193	Thr Phe Leu Glu Arg Ile Ser Gly Pro Arg Ile Ala Gly Thr Val Phe	
194	430 435 440	
196	tct tgg aca cac cgt agt gcc agc cct act aat gaa gta agt cca tct	1637
197	Ser Trp Thr His Arg Ser Ala Ser Pro Thr Asn Glu Val Ser Pro Ser	
198	445 450 455	
200	aga att aca caa att cca tgg gta aag gcg cat act ctt gca tct ggt	1685

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201 Arg Ile Thr Gln Ile Pro Trp Val Lys Ala His Thr Leu Ala Ser Gly			
202 460	465	470	
204 gcc tcc gtc att aaa ggt cct gga ttt aca ggt gga gat att ctg act			1733
205 Ala Ser Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Thr			
206 475	480	485	490
208 agg aat agt atg ggc gag ctg ggg acc tta cga gta acc ttc aca gga			1781
209 Arg Asn Ser Met Gly Glu Leu Gly Thr Leu Arg Val Thr Phe Thr Gly			
210 495	500	505	
212 aga tta cca caa agt tat tat ata cgt ttc cgt tat gct tcg gta gca			1829
213 Arg Leu Pro Gln Ser Tyr Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala			
214 510	515	520	
216 aat agg agt ggt aca ttt aga tat tca cag cca cct tcg tat gga att			1877
217 Asn Arg Ser Gly Thr Phe Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile			
218 525	530	535	
220 tca ttt cca aaa act atg gac gca ggt gaa cca cta aca tct cgt tcg			1925
221 Ser Phe Pro Lys Thr Met Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser			
222 540	545	550	
224 ttc gct cat aca aca ctc ttc act cca ata acc ttt tca cga gct caa			1973
225 Phe Ala His Thr Thr Leu Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln			
226 555	560	565	570
228 gaa gaa ttt gat cta tac atc caa tcg ggt gtt tat ata gat cga att			2021
229 Glu Glu Phe Asp Leu Tyr Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile			
230 575	580	585	
232 gaa ttt ata ccg gtt act gca aca ttt gag gca gaa tat gat tta gaa			2069
233 Glu Phe Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu			
234 590	595	600	
236 aga gcg caa aag gtg gtg aat gcc ctg ttt acg tct aca aac caa cta			2117
237 Arg Ala Gln Lys Val Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu			
238 605	610	615	
240 ggg cta aaa aca gat gtg acg gat tat cat att gat cag gta tcc aat			2165
241 Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn			
242 620	625	630	
244 cta gtt gcg tgt tta tcg gat gaa ttt tgt ctg gat gaa aag aga gaa			2213
245 Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu			
246 635	640	645	650
248 ttg tcc gag aaa gtt aaa cat gca aag cga ctc agt gat gag cgg aat			2261
249 Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn			
250 655	660	665	
252 tta ctt caa gat cca aac ttc aga ggg atc aat agg caa cca gac cgt			2309
253 Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg			
254 670	675	680	
256 ggc tgg aga gga agt acg gat att act atc caa gga gga gat gac gta			2357
257 Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val			
258 685	690	695	
260 ttc aaa gag aat tac gtt acg cta ccg ggt acc ttt gat gag tgc tat			2405
261 Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr			
262 700	705	710	
264 cca acg tat tta tat caa aaa ata gat gag tcg aaa tta aaa gcc tat			2453
265 Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr			

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266	715	720	725	730	
268	acc cgt tat caa tta aga ggg tat atc gaa gat agt caa gac tta gaa				2501
269	Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu				
270	735	740	745		
272	atc tat tta att cgt tac aat gca aaa cac gaa ata gta aat gta cca				2549
273	Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro				
274	750	755	760		
276	ggt aca gga agt tta tgg cct ctt tct gta gaa aat caa att gga cct				2597
277	Gly Thr Gly Ser Leu Trp Pro Leu Ser Val Glu Asn Gln Ile Gly Pro				
278	765	770	775		
280	tgt gga gaa ccg aat cga tgc gcg cca cac ctt gaa tgg aat cct gat				2645
281	Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp				
282	780	785	790		
284	tta cac tgt tcc tgc aga gac ggg gaa aaa tgt gca cat cat tct cat				2693
285	Leu His Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His				
286	795	800	805	810	
288	cat ttc tct ttg gac att gat gtt gga tgt aca gac tta aat gag gac				2741
289	His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp				
290	815	820	825		
292	tta ggt gta tgg gtg ata ttc aag att aag acg caa gat ggc cac gca				2789
293	Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala				
294	830	835	840		
296	cga cta ggg aat cta gag ttt ctc gaa gag aaa cca tta tta gga gaa				2837
297	Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu				
298	845	850	855		
300	gca cta gct cgt gtg aaa aga gcg gag aaa aaa tgg aga gac aaa cgc				2885
301	Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg				
302	860	865	870		
304	gaa aca tta caa ttg gaa aca act atc gtt tat aaa gag qca aaa gaa				2933
305	Glu Thr Leu Gln Leu Glu Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu				
306	875	880	885	890	
308	tct gta gat gct tta ttt gta aac tct caa tat gat aga tta caa gcg				2981
309	Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala				
310	895	900	905		
312	gat acg aac atc gcg atg att cat gcg gca gat aaa cgc gtt cat aga				3029
313	Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg				
314	910	915	920		
316	att cga gaa gcg tat ctg ccg gag ctg tct gtg att ccg ggt gtc aat				3077
317	Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn				
318	925	930	935		
320	gcg gct att ttt gaa gaa tta gaa gag cgt att ttc act gca ttt tcc				3125
321	Ala Ala Ile Phe Glu Glu Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser				
322	940	945	950		
324	cta tat gat gcg aga aat att att aaa aat ggc gat ttc aat aat ggc				3173
325	Leu Tyr Asp Ala Arg Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly				
326	955	960	965	970	
328	tta tta tgc tgg aac gtg aaa ggg cat gta gag gta gaa gaa caa aac				3221
329	Leu Leu Cys Trp Asn Val Lys Gly His Val Glu Val Glu Glu Gln Asn				
330	975	980	985		

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